
CLAIMS LISTING

1. (Currently Amended) A method of analyzing gene expressions comprising acts of:
determining a first gene expression pattern for a first condition, wherein the first
5 gene expression pattern comprises a gene expression;
forming a first spatial-expression pattern by:
selecting a chromosomal region having ~~a length and an exon having a start~~
~~and a stop position~~; and
associating the gene expression within the first gene expression pattern
10 with its corresponding exon ~~by~~:
~~determining, within the chromosomal region, the start and stop position of~~
~~the exon; and~~
~~associating the gene expression to the first spatial-expression pattern for~~
~~the length between the start and stop position of the exon; and~~
15 wherein the act of forming the first spatial-expression pattern further
comprises an act of creating a first spatial-expression pattern signal wherein the
first spatial-expression pattern signal is a representation of the first spatial-
expression pattern where a magnitude of the first spatial-expression pattern signal
at any point is determined by an expression level of the corresponding exon.

20 2. (Cancelled)

3. (Currently Amended) The method of claim 1 [[2]], wherein:

the magnitude of the first spatial-expression pattern signal at points spanning the
25 chromosomal region are a function of the expression level of an exon at corresponding
positions in the chromosomal region.

4. (Currently Amended) The method of claim 1 [[2]], further comprising an act of:

identifying first regular spatial patterns in the first spatial-expression pattern
30 signal.

5. (Withdrawn) The method of claim 4, wherein
the act of identifying first regular spatial patterns in the first spatial-expression
pattern signal is performed through the use of Fourier transform signal processing.

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6. (Withdrawn) The method of claim 5, further comprising an act of:
identifying a group of genes contributing to local maximum points of the
generated Fourier transform spectrum.

10 7. (Original) The method of claim 4, wherein
the act of identifying first regular spatial patterns in the first spatial-expression
pattern signal is performed through the use of Wavelet transform signal processing.

15 8. (Original) The method of claim 7, further comprising an act of:
identifying a group of genes contributing to local maximum points of the
generated Wavelet transformed signal at different scales and positions.

20 9. (Original) The method of claim 4, wherein:
the act of identifying first regular spatial patterns in the first spatial-expression
pattern signal identifies a set of genes.

25 10. (Original) The method of claim 9, wherein:
the act of identifying first regular spatial patterns in the first spatial-expression
pattern signal identifies a set of genes which participate in a common biological process
or function.

11. (Original) The method of claim 1, further comprising acts of:
determining a second gene expression pattern for a second condition, wherein the
second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern
with its corresponding exon.

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12. (Original) The method of claim 11, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern
signal;

identifying second regular spatial patterns in the second spatial-expression pattern
signal; and

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comparing the first and second regular spatial patterns.

13. (Original) The method of claim 11, further comprising an act of:

repeating the steps of determining a gene expression pattern and forming a
spatial-expression pattern signal for any number of gene expression patterns.

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14. (Original) The method of claim 13, further comprising acts of:

comparing all formed spatial-expression pattern signals.

20 15. (Original) The method of claim 14, wherein:

the act of comparing all formed spatial-expression pattern signals involves
clustering all formed spatial-expression pattern signals.

16. (Original) The method of claim 15, further comprising acts of:

25 identifying gene groups contributing to the differences in significant changes in
the first and second regular spatial-expression pattern signals.

17. (Original) The method of claim 1, wherein the chromosomal region is an entire
chromosome.

18. (Original) The method of claim 11, wherein:

the first spatial-expression pattern and the second-expression pattern are selected from different chromosomes.

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19. (Original) The method of claim 11, wherein:

the first spatial-expression and the second-expression pattern are selected from different genomes.

10 20. (Currently Amended) An apparatus for analyzing gene expressions, the apparatus comprising a computer system including a processor, a memory coupled with the processor, an input coupled with the processor for receiving input data, and an output coupled with the processor for outputting data, wherein the computer system further comprises means, residing in its processor and memory, for:

15 determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having ~~a length and an exon having a start and a stop position~~; and

20 associating the gene expression within the first gene expression pattern with its corresponding exon by:

~~determining, within the chromosomal region, the start and stop position of the exon; and~~

25 ~~associating the gene expression to the first spatial-expression pattern for the length between the start and stop position of the exon; and~~

wherein the means for forming the first spatial-expression pattern further comprises means for creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-

expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

21. (Cancelled)

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22. (Currently Amended) An apparatus as set forth in claim 20 [[21]], wherein:

the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

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23. (Currently Amended) An apparatus as set forth in claim 20 [[21]], further comprising an means for:

identifying first regular spatial patterns in the first spatial-expression pattern signal.

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24. (Withdrawn) An apparatus as set forth in claim 23, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

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25. (Withdrawn) An apparatus as set forth in claim 24, further comprising an means for:

identifying a group of genes contributing to local maximum points of the generated Fourier transform spectrum.

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26. (Original) An apparatus as set forth in claim 23, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

27. (Original) An apparatus as set forth in claim 26, further comprising an means for:
identifying a group of genes contributing to local maximum points of the
generated Wavelet transformed signal at different scales and positions.

5 28. (Original) An apparatus as set forth in claim 23, wherein:
the means for identifying first regular spatial patterns in the first spatial-
expression pattern signal identifies a set of genes.

29. (Original) An apparatus as set forth in claim 28, wherein:
10 the means for identifying first regular spatial patterns in the first spatial-
expression pattern signal identifies a set of genes which participate in a common
biological process or function.

30. (Original) An apparatus as set forth in claim 20, further comprising acts of:
15 determining a second gene expression pattern for a second condition, wherein
the second gene expression pattern comprises a gene expression; and
forming a second spatial-expression pattern by:
selecting a chromosomal region having an exon; and
associating a gene expression within the second gene expression
20 pattern with its corresponding exon.

31. (Original) An apparatus as set forth in claim 30, further comprising acts of:
identifying first regular spatial patterns in the first spatial-expression pattern
signal;
25 identifying second regular spatial patterns in the second spatial-expression
pattern signal; and
comparing the first and second regular spatial patterns.

32. (Original) An apparatus as set forth in claim 31, further comprising an means for:

repeating the steps of determining a gene expression pattern and forming a spatial-expression pattern signal for any number of gene expression patterns.

33. (Original) An apparatus as set forth in claim 30, further comprising acts of:

5 comparing all formed spatial-expression pattern signals.

34. (Original) An apparatus as set forth in claim 33, wherein:

 the means for comparing all formed spatial-expression pattern signals
involves clustering all formed spatial-expression pattern signals.

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35. (Original) An apparatus as set forth in claim 34 further comprising acts of:

 identifying gene groups contributing to the differences in significant changes
in the first and second regular spatial-expression pattern signals.

15 36. (Original) An apparatus as set forth in claim 20, wherein the chromosomal region is
an entire chromosome.

37. (Previously Presented) An apparatus as set forth in claim 30, wherein:

 the first spatial-expression pattern and the second-expression pattern are
20 selected from different chromosomes.

38. (Original) An apparatus as set forth in claim 30, wherein:

 the first spatial-expression and the second-expression pattern are selected
from different genomes.

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39. (Currently Amended) A computer program product for analyzing gene expressions,
the computer program product comprising means, encoded in a computer-readable
medium for:

determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;
forming a first spatial-expression pattern by:
selecting a chromosomal region having ~~a length and an exon having a start~~
5 ~~and a stop position~~; and
associating the gene expression within the first gene expression pattern with its corresponding exon by:
~~determining, within the chromosomal region, the start and stop position of the exon; and~~
10 ~~associating the gene expression to the first spatial-expression pattern for the length between the start and stop position of the exon; and~~
wherein the means for forming the first spatial-expression pattern further comprises means for creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-
15 expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

40. (Cancelled)

20 41. (Currently Amended) A computer program product as set forth in claim 39 ~~[[40]]~~, wherein:
the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

25 42. (Currently Amended) A computer program product as set forth in claim 39 ~~[[40]]~~, further comprising an means for:
identifying first regular spatial patterns in the first spatial-expression pattern signal.

43. (Withdrawn) A computer program product as set forth in claim 42, wherein
the means for identifying first regular spatial patterns in the first spatial-
expression pattern signal is performed through the use of Fourier transform signal
5 processing.

44. (Withdrawn) A computer program product as set forth in claim 43, further
comprising an means for:
identifying a group of genes contributing to local maximum points of the
10 generated Fourier transform spectrum.

45. (Original) A computer program product as set forth in claim 42, wherein
the means for identifying first regular spatial patterns in the first spatial-
expression pattern signal is performed through the use of Wavelet transform signal
15 processing.

46. (Original) A computer program product as set forth in claim 45, further comprising
an means for:
identifying a group of genes contributing to local maximum points of the
20 generated Wavelet transformed signal at different scales and positions.

47. (Original) A computer program product as set forth in claim 42, wherein:
the means for identifying first regular spatial patterns in the first spatial-
expression pattern signal identifies a set of genes.
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48. (Original) A computer program product as set forth in claim 47, wherein:
the means for identifying first regular spatial patterns in the first spatial-
expression pattern signal identifies a set of genes which participate in a common
biological process or function.

49. (Original) A computer program product as set forth in claim 39, further comprising acts of:

5 determining a second gene expression pattern for a second condition, wherein
the second gene expression pattern comprises a gene expression; and
 forming a second spatial-expression pattern by:
 selecting a chromosomal region having an exon; and
 associating a gene expression within the second gene expression pattern
with its corresponding exon.

10 50. (Original) A computer program product as set forth in claim 49, further comprising acts of:

 identifying first regular spatial patterns in the first spatial-expression pattern
signal;
15 identifying second regular spatial patterns in the second spatial-expression
pattern signal; and
 comparing the first and second regular spatial patterns.

20 51. (Original) A computer program product as set forth in claim 50, further comprising an means for:

 repeating the steps of determining a gene expression pattern and forming a
spatial-expression pattern signal for any number of gene expression patterns.

25 52. (Original) A computer program product as set forth in claim 49, further comprising acts of:

 comparing all formed spatial-expression pattern signals.

53. (Original) A computer program product as set forth in claim 52, wherein:

the means for comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

54. (Original) A computer program product as set forth in claim 53, further comprising
5 acts of:

identifying gene groups contributing to the differences in significant changes in the first and second regular spatial-expression pattern signals.

55. (Previously Presented) A computer program product as set forth in claim 39, wherein
10 the chromosomal region is an entire chromosome.

56. (Original) A computer program product as set forth in claim 39, wherein:
the first spatial-expression pattern and the second-expression pattern are selected from different chromosomes.

15 57. (Original) A computer program product as set forth in claim 39, wherein:
the first spatial-expression and the second-expression pattern are selected from different genomes.

20 58. (Currently Amended) A method of analyzing gene expressions comprising acts of:
determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;
forming a first spatial-expression pattern by:
selecting a chromosomal region having a length and an exon having a start
25 and stop position;
associating the gene expression within the first gene expression pattern with its corresponding exon by:
determining, within the chromosomal region, the start and stop position of the exon; and

associating the gene expression to the first spatial-expression
pattern for the length between the start and stop position of the exon; and
creating a first spatial-expression pattern signal wherein the first spatial-
expression pattern signal is a representation of the first spatial-expression pattern
5 where a magnitude of the first spatial-expression pattern signal at any point is
determined by an expression level of the corresponding exon.

59. (Original) The method of claim 58, further comprising an act of:
identifying first regular spatial patterns in the first spatial-expression pattern
10 signal.

60. (Withdrawn) The method of claim 59, wherein
the act of identifying first regular spatial patterns in the first spatial-expression
pattern signal is performed through the use of Fourier transform signal processing.

15 61. (Original) The method of claim 59, wherein
the act of identifying first regular spatial patterns in the first spatial-expression
pattern signal is performed through the use of Wavelet transform signal processing.

20 62. (Original) The method of claim 58, further comprising acts of:
determining a second gene expression pattern for a second condition, wherein
the second gene expression pattern comprises a gene expression; and
forming a second spatial-expression pattern by:
selecting a chromosomal region having an exon; and
25 associating a gene expression within the second gene expression pattern
with its corresponding exon.

63. (Original) The method of claim 62, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern signal;

identifying second regular spatial patterns in the second spatial-expression pattern signal; and

5 comparing the first and second regular spatial patterns.

64. (Original) The method of claim 62, further comprising acts of:

comparing all formed spatial-expression pattern signals.

10 65. (Original) The method of claim 64, wherein:

the act of comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

66. (Currently Amended) An apparatus for analyzing gene expressions, the apparatus

15 comprising a computer system including a processor, a memory coupled with the processor, an input coupled with the processor for receiving input data, and an output coupled with the processor for outputting data, wherein the computer system further comprises means, residing in its processor and memory, for:

20 determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having ~~a length~~ and an exon having ~~a start and a stop position~~;

25 associating the gene expression within the first gene expression pattern with its corresponding exon by:

~~determining, within the chromosomal region, the start and stop position of the exon;~~

~~associating the gene expression to the first spatial-expression pattern for the length between the start and stop position of the exon; and~~

creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

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67. (Original) An apparatus as set forth in claim 66, further comprising an means for:
identifying first regular spatial patterns in the first spatial-expression pattern signal.

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68. (Withdrawn) An apparatus as set forth in claim 67, wherein
the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

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69. (Original) An apparatus as set forth in claim 67, wherein
the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

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70. (Previously Presented) An apparatus as set forth in claim 66, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

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selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern with its corresponding exon.

71. (Previously Presented) An apparatus as set forth in claim 66, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern signal;

5 identifying second regular spatial patterns in the second spatial-expression pattern signal; and

comparing the first and second regular spatial patterns.

72. (Previously Presented) An apparatus as set forth in claim 66, further comprising acts of:

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comparing all formed spatial-expression pattern signals.

73. (Previously Presented) An apparatus as set forth in claim 72, wherein:

the means for comparing all formed spatial-expression pattern signals

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involves clustering all formed spatial-expression pattern signals.

74. (Currently Amended) A computer program product for analyzing gene expressions, the computer program product comprising means, encoded in a computer-readable medium for:

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determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having ~~a length and an exon having a start and a stop position;~~

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associating the gene expression within the first gene expression pattern with its corresponding exon, ~~by:~~

~~determining, within the chromosomal region, the start and stop position of the exon; and~~

~~associating the gene expression to the first spatial-expression~~
~~pattern for the length between the start and stop position of the exon; and~~
creating a first spatial-expression pattern signal wherein the first spatial-
expression pattern signal is a representation of the first spatial-expression pattern
5 where a magnitude of the first spatial-expression pattern signal at any point is
determined by an expression level of the corresponding exon.

75. (Original) A computer program product as set forth in claim 74, further comprising
an means for:

10 identifying first regular spatial patterns in the first spatial-expression pattern
signal.

76. (Withdrawn) A computer program product as set forth in claim 75, wherein
the means for identifying first regular spatial patterns in the first spatial-
15 expression pattern signal is performed through the use of Fourier transform signal
processing.

77. (Original) A computer program product as set forth in claim 75, wherein
the means for identifying first regular spatial patterns in the first spatial-
20 expression pattern signal is performed through the use of Wavelet transform signal
processing.

78. (Original) A computer program product as set forth in claim 74, further comprising
acts of:

25 determining a second gene expression pattern for a second condition, wherein
the second gene expression pattern comprises a gene expression; and
forming a second spatial-expression pattern by:
selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern with its corresponding exon.

79. (Original) A computer program product as set forth in claim 78, further comprising
5 acts of:

identifying first regular spatial patterns in the first spatial-expression pattern signal;

identifying second regular spatial patterns in the second spatial-expression pattern signal; and

10 comparing the first and second regular spatial patterns.

80. (Original) A computer program product as set forth in claim 78, further comprising acts of:

comparing all formed spatial-expression pattern signals.

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81. (Previously Presented) A computer program product as set forth in claim 80, wherein:

the means for comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

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